

O. B. S.

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/075,074

DATE: 03/01/2002 8:55
TIME: 11:45:05

Input Set : A:\EP.txt
Output Set: N:\CRF3\03012002\J075074.raw

3 <110> APPLICANT: Brown, Arthur
 4 Wible, Barbara
 5 Yang, Qing
 7 <120> TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on
 Cell Surfaces
 8 and Nucleic Acids That Encode The Same
 10 <130> FILE REFERENCE: 22884/04066
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/075,074
 C--> 12 <141> CURRENT FILING DATE: 2002-12-13
 12 <150> PRIOR APPLICATION NUMBER: 09/062,440
 13 <151> PRIOR FILING DATE: 1998-04-17
 15 <150> PRIOR APPLICATION NUMBER: 09/712,495
 16 <151> PRIOR FILING DATE: 2000-11-14
 18 <160> NUMBER OF SEQ ID NOS: 13
 20 <170> SOFTWARE: PatentIn version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1725
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Rattus norvegicus
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(1725)
 31 <400> SEQUENCE: 1
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 33 Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu
 34 1 5 10 15
 36 ggg cct tcc gat ctc tct ttg ctc tct ttg ccc cct ggc acc tct cct 96
 37 Gly Pro Ser Asp Leu Ser Leu Ser Leu Pro Pro Gly Thr Ser Pro
 38 20 25 30
 40 gta ggc tcc ccc agc ccc ctt gct tcc att cct ccc acc ctc ctg acc 144
 41 Val Gly Ser Pro Ser Pro Leu Ala Ser Ile Pro Pro Thr Leu Leu Thr
 42 35 40 45
 44 cct ggc acc ttg ctg ggc cct aag cgt gag gtg gac atg cac cct cct 192
 45 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
 46 50 55 60
 48 ctg ccc cag cct gtg cac cct gac gtc acc atg aaa cca ctg ccc ttc 240
 49 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
 50 65 70 75 80
 52 tac gaa gtc tac gga gag ctc atc cgg ccg acc acc ctt gcg tcc acc 288
 53 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
 54 85 90 95
 56 tcc agt cag agg ttt gag gaa gcc cac ttt acc ttt gca ctc act ccc 336
 57 Ser Ser Gln Arg Phe Glu Ala His Phe Thr Phe Ala Leu Thr Pro
 58 100 105 110

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60	cag cag ctg cag cag att ctc aca tcc agg gag gtt ctg cca gga gcc	384
61	Gln Gln Leu Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala	
62	115 120 125	
64	aag tgc gat tat acc ata caa gtg cag ctc agg ttc tgt ctc tgt gag	432
65	Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu	
66	130 135 140	
68	acc agc tgc ccc cag gag gac tat ttc ccc cct aac ctc ttt gtc aag	480
69	Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys	
70	145 150 155 160	
72	gtt aat ggg aaa ctc tgc ccc ctg ccg ggt tac ctc cct cca acc aag	528
73	Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys	
74	165 170 175	
76	aat gga gct gag ccc aag agg cct agt cgt cca atc aac atc aca ccc	576
77	Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro	
78	180 185 190	
80	ctg gct cgt ctc tca gcc act gtt ccc aac acc ata gtg gtt aac tgg	624
81	Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp	
82	195 200 205	
84	tca tct gag ttt gga cgg aat tac tcc ttg tct gtg tac ctg gtg agg	672
85	Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg	
86	210 215 220	
88	cag ttg act gca ggg acc ctg cta caa aag ctc aga gcc aag ggt atc	720
89	Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile	
90	225 230 235 240	
92	cgg aat cca gac cat tcc cga gca ctg atc aag gag aaa ttg act gct	768
93	Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala	
94	245 250 255	
96	gac ccc gac agt gaa gtg gct act aca agt ctc cgg gtg tca ctc atg	816
97	Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met	
98	260 265 270	
100	tgc ccg ctg ggg aag atg cgc ctg act gtc cca tgc cgc gct ctc acc	864
101	Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr	
102	275 280 285	
104	tgt gcc cac ctg cag agt ttc gat gct gcc ctt tat cta cag atg aat	912
105	Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn	
106	290 295 300	
108	gag aaa aag cca aca tgg acg tgc cct gtg tgt gac aag aag gct ccc	960
109	Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro	
110	305 310 315 320	
112	tat gag tca ctg att att gat ggt tta ttc atg gaa att ctt aat tcc	1008
113	Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Asn Ser	
114	325 330 335	
116	tgt tcg gat tgt gat gag atc cag ttc atg gaa gat gga tcc tgg tgt	1056
117	Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys	
118	340 345 350	
120	cca atg aaa ccc aag aag gag gca tcc gag gtt tgc ccc cca cca ggg	1104
121	Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly	
122	355 360 365	
124	tat ggg ctg gat ggt ctc cag tat agc cca gtc cag gag gga aat cag	1152

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125	Tyr	Gly	Leu	Asp	Gly	Leu	Gln	Tyr	Ser	Pro	Val	Gln	Glu	Gly	Asn	Gln			
126	370					375						380							
128	tca	gag	aat	aag	aag	agg	gtt	gaa	gtc	att	gac	ttg	aca	atc	gaa	agc	1200		
129	Ser	Glu	Asn	Lys	Lys	Arg	Val	Glu	Val	Ile	Asp	Leu	Thr	Ile	Glu	Ser			
130	385					390						395				400			
132	tca	tca	gat	gag	gaa	gat	ctg	ccc	ccc	acc	aag	cac	tgc	cct	gtt		1248		
133	Ser	Ser	Asp	Glu	Glu	Asp	Leu	Pro	Pro	Thr	Lys	Lys	His	Cys	Pro	Val			
134						405					410				415				
136	acc	tcg	gct	gcc	att	cca	gcc	ctt	cct	gga	agc	aaa	gga	gcc	ctg	acc	1296		
137	Thr	Ser	Ala	Ala	Ile	Pro	Ala	Leu	Pro	Gly	Ser	Lys	Gly	Ala	Leu	Thr			
138						420					425				430				
140	tct	ggt	cac	cag	ccg	tct	tcg	gtg	ctg	cg	agc	cct	gca	atg	gg	aca	1344		
141	Ser	Gly	His	Gln	Pro	Ser	Ser	Val	Leu	Arg	Ser	Pro	Ala	Met	Gly	Thr			
142						435					440				445				
144	ctg	ggc	agt	gat	tcc	ctg	tct	agt	ctc	cca	cta	cat	gag	tac	cca	cct	1392		
145	Leu	Gly	Ser	Asp	Phe	Leu	Ser	Ser	Leu	Pro	Leu	His	Glu	Tyr	Pro	Pro			
146						450					455				460				
148	gcc	tcc	ccg	ctg	ggg	gct	gac	atc	caa	gg	tta	gat	tta	ttt	tct	tcc	1440		
149	Ala	Phe	Pro	Leu	Gly	Ala	Asp	Ile	Gln	Gly	Leu	Asp	Leu	Phe	Ser	Phe			
150	465					470					475				480				
152	c	tt	c	ag	act	gag	agt	cag	cac	tac	agc	cct	tca	gtt	atc	act	tca	cta	1488
153	Leu	Gln	Thr	Glu	Ser	Gln	His	Tyr	Ser	Pro	Ser	Val	Ile	Thr	Ser	Leu			
154						485					490				495				
156	gat	gag	cag	gac	acc	ctt	ggc	cac	tcc	caa	tcc	gg	gga	acc	cct		1536		
157	Asp	Glu	Gln	Asp	Thr	Leu	Gly	His	Phe	Phe	Gln	Phe	Arg	Gly	Thr	Pro			
158						500					505				510				
160	ccc	cac	tcc	ctg	ggc	cca	ctg	gcc	ccc	aca	ttg	ggg	agc	tct	cac	cgc	1584		
161	Pro	His	Phe	Leu	Gly	Pro	Leu	Ala	Pro	Thr	Leu	Gly	Ser	Ser	His	Arg			
162						515					520				525				
164	agc	gcc	act	cca	gca	ccc	gct	cct	ggc	cgt	gtc	agc	agc	att	gtg	gct	1632		
165	Ser	Ala	Thr	Pro	Ala	Pro	Ala	Pro	Gly	Arg	Val	Ser	Ser	Ile	Val	Ala			
166						530					535				540				
168	cct	ggg	agt	tcc	ttg	agg	gaa	ggg	cat	gga	gga	ccc	ctg	cct	tcc	gg	1680		
169	Pro	Gly	Ser	Ser	Leu	Arg	Glu	Gly	His	Gly	Gly	Pro	Leu	Pro	Ser	Gly			
170	545					550					555				560				
172	ccc	tct	ttg	act	ggc	tgt	cg	tca	gac	gtc	att	tcc	ttg	gac	tga		1725		
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188	Gly	Pro	Ser	Asp	Leu	Ser	Leu	Leu	Ser	Leu	Pro	Pro	Gly	Thr	Ser	Pro			
189						20					25				30				
192	Val	Gly	Ser	Pro	Ser	Pro	Leu	Ala	Ser	Ile	Pro	Pro	Thr	Leu	Leu	Thr			
193						35					40				45				

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196 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
197 50 55 60
200 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
201 65 70 75 80
204 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
205 85 90 95
208 Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
209 100 105 110
212 Gln Gln Leu Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala
213 115 120 125
216 Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu
217 130 135 140
220 Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys
221 145 150 155 160
224 Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys
225 165 170 175
228 Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro
229 180 185 190
232 Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp
233 195 200 205
236 Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg
237 210 215 220
240 Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile
241 225 230 235 240
244 Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala
245 245 250 255
248 Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met
249 260 265 270
252 Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr
253 275 280 285
256 Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn
257 290 295 300
260 Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro
261 305 310 315 320
264 Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Asn Ser
265 325 330 335
268 Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys
269 340 345 350
272 Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly
273 355 360 365
276 Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Glu Gly Asn Gln
277 370 375 380
280 Ser Glu Asn Lys Lys Arg Val Glu Val Ile Asp Leu Thr Ile Glu Ser
281 385 390 395 400
284 Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Pro Val
285 405 410 415
288 Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Ala Leu Thr
289 420 425 430
292 Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr

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293	435	440	445														
296	Leu	Gly	Ser	Asp	Phe	Leu	Ser	Ser	Leu	Pro	Leu	His	Glu	Tyr	Pro	Pro	
297	450															460	
300	Ala	Phe	Pro	Leu	Gly	Ala	Asp	Ile	Gln	Gly	Leu	Asp	Leu	Phe	Ser	Phe	
301	465															475	
304	Leu	Gln	Thr	Glu	Ser	Gln	His	Tyr	Ser	Pro	Ser	Val	Ile	Thr	Ser	Leu	
305																495	
308	Asp	Glu	Gln	Asp	Thr	Leu	Gly	His	Phe	Phe	Gln	Phe	Arg	Gly	Thr	Pro	
309																510	
312	Pro	His	Phe	Leu	Gly	Pro	Leu	Ala	Pro	Thr	Leu	Gly	Ser	Ser	His	Arg	
313																525	
316	Ser	Ala	Thr	Pro	Ala	Pro	Ala	Pro	Gly	Arg	Val	Ser	Ser	Ile	Val	Ala	
317																540	
320	Pro	Gly	Ser	Ser	Leu	Arg	Glu	Gly	His	Gly	Gly	Pro	Leu	Pro	Ser	Gly	
321	545															560	
324	Pro	Ser	Leu	Thr	Gly	Cys	Arg	Ser	Asp	Val	Ile	Ser	Leu	Asp			
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333	<220>	FEATURE:															
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335	<222>	LOCATION:	(1)..(1725)														
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339	Met	Lys	Ile	Lys	Glu	Leu	Tyr	Arg	Arg	Arg	Phe	Pro	Arg	Lys	Thr	Leu	
340	1															15	
342	ggg	ccc	tct	gat	ctc	tcc	ctc	tct	ttg	ccc	cct	ggc	acc	tct	cct		96
343	Gly	Pro	Ser	Asp	Leu	Ser	Leu	Leu	Ser	Leu	Pro	Pro	Gly	Thr	Ser	Pro	
344																30	
346	gta	ggc	tcc	cct	ggt	cct	cta	gct	ccc	att	ccc	cca	acg	ctg	ttg	gcc	144
347	Val	Gly	Ser	Pro	Gly	Pro	Leu	Ala	Pro	Ile	Pro	Pro	Thr	Leu	Leu	Ala	
348																45	
350	cct	ggc	acc	ctg	ctg	ggc	ccc	aag	cgt	gag	gtg	gac	atg	cac	ccc	cct	192
351	Pro	Gly	Thr	Leu	Leu	Gly	Pro	Lys	Arg	Glu	Val	Asp	Met	His	Pro	Pro	
352																60	
354	ctg	ccc	cag	cct	gtg	cac	cct	gat	gtc	acc	atg	aaa	cca	ttg	ccc	ttc	240
355	Leu	Pro	Gln	Pro	Val	His	Pro	Asp	Val	Thr	Met	Lys	Pro	Leu	Pro	Phe	
356																80	
358	tat	gaa	gtc	tat	ggg	gag	ctc	atc	cgg	ccc	acc	acc	ctt	gca	tcc	act	288
359	Tyr	Glu	Val	Tyr	Gly	Glu	Leu	Ile	Arg	Pro	Thr	Thr	Leu	Ala	Ser	Thr	
360																95	
362	tct	agc	cag	cg	ttt	gag	gaa	g	cg	cac	ttt	gcc	ctc	aca	ccc		336
363	Ser	Ser	Gln	Arg	Phe	Glu	Glu	Ala	His	Phe	Thr	Phe	Ala	Leu	Thr	Pro	
364																110	
366	cag	caa	gtg	cag	cag	att	ctt	aca	tcc	aga	gag	gtt	ctg	cca	gga	gcc	384
367	Gln	Gln	Val	Gln	Gln	Ile	Leu	Thr	Ser	Arg	Glu	Val	Leu	Pro	Gly	Ala	
368																125	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 03/01/2002
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:864 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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L:1039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1048 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
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L:1160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11